

SEQUENCE LISTING

<110> SIREEN AG

<120> Methods of identifying, selecting and/or characterizing compounds which modulate the activity of a Src family kinase

<130> SI07P001WO

<150> EP 03028713.0

<151> 2003-12-12

<160> 51

<170> PatentIn version 3.1

<210> 1

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Description of sequence: Src-KA

<400> 1

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Ala Thr Leu Lys Pro Gly Thr
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 2
<211> 536
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: Src-TQ

<400> 2

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe

50

55

60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335

Ile Tyr Ile Val Gln Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 3
<211> 536
<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Src-YF

<400> 3

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg

465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525

Gln Phe Gln Pro Gly Glu Asn Leu
 530 535

<210> 4

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Src-TQ/YF

<400> 4

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335

Ile Tyr Ile Val Gln Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
515 520 525

Gln Phe Gln Pro Gly Glu Asn Leu
530 535

<210> 5
<211> 543
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: Yes-KA

<400> . 5

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
 115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile

12/103

290	295	300
Ala Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu		
305	310	315 320
Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr		
	325	330 335
Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser		
	340	345 350
Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu		
	355	360 365
Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met		
	370	375 380
Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala		
	385	390 395 400
Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly		
	405	410 415
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala		
	420	425 430
Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg		
	435	440 445
Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu		
	450	455 460
Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu		
	465	470 475 480
Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly		
	485	490 495
Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp		
	500	505 510
Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp		
	515	520 525
Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu		
	530	535 540

<210> 6
 <211> 543
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Yes-TQ

<400> 6

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
 115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe Met Ser
340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 7

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Yes-YF

<400> 7

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp

115

120

125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 8
 <211> 543
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Yes-TQ/YF

<400> 8

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe Met Ser
 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu

530

535

540

<210> 9
 <211> 529
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> Description of sequence: Fgr-KA

<400> 9

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
 180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
 275 280 285

Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
 290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
 305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe
 325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
 340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
 355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
 370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
 385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
 420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln
 515 520 525

Thr

<210> 10
 <211> 529
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Fgr-TQ

<400> 10

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
 180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
 275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser ~~Phe~~ Ala Phe Leu
 290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
 305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe
 325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
 340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu

355

360

365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
 370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
 385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
 420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln
 515 520 525

Thr

<210> 11
 <211> 529
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Fgr-YF

<400> 11

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
 180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe
325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
450 455 460

Arg-Glu Val-Leu-Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln
515 520 525

Thr

<210> 12

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fgr-TQ/YF

<400> 12

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Glu ~~Leu Thr~~ Gly Cys Ile
115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly

28/103

180

185

190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
 275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
 290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
 305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe
 325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
 340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
 355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
 370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
 385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
 420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln
 515 520 525

Thr

<210> 13
 <211> 537
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Fyn-KA

<400> 13

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
 85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
 115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
 130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
 145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
 165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
 180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
 195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
 210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
 225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
 245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
 260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Ala Thr Leu Lys Pro Gly
 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335

Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 14
<211> 537
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: Fyn-TQ

<400> 14

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu

1	5	10	15
Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr	20	25	30
Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro	35	40	45
Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe	50	55	60
Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly	65	70	75
Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg	85	90	95
Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu	100	105	110
Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly	115	120	125
Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile	130	135	140
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu	145	150	155
Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg	165	170	175
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp	180	185	190
Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu	195	200	205
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu	210	215	220
Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys	225	230	235
Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu	245	250	255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
 260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335

Pro Ile Tyr Ile Val Gln Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 15

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fyn-YF

<400> 15

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
 85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
 115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
 130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
 145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
 165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
 180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
 195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
 210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
 225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
 245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
 260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335

Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys ~~Leu~~ ~~Asn~~ Leu Val
 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp

420 425 430
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445
 Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460
 Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480
 Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495
 Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510
 Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525
 Pro Gln Phe Gln Pro Gly Glu Asn Leu
 530 535

 <210> 16
 <211> 537
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> Description of sequence: Fyn-TQ/YF

 <400> 16
 Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
 1 5 10 15
 Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
 20 25 30
 Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
 35 40 45
 Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
 50 55 60
 Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
325 330 335

Pro Ile Tyr Ile Val Gln Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525

Pro Gln Phe Gln Pro Gly Glu Asn Leu
 530 535

<210> 17
 <211> 509
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Lck-KA

<400> 17

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
 145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
 165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn ~~Leu Ser Phe Thr Gly~~ Phe Tyr
 180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
 195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
 210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
 225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe

245	250	255
Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val		
260	265	270
Ala Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu		
275	280	285
Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr		
290	295	300
Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu		
305	310	315
Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu		
325	330	335
Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met		
340	345	350
Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala		
355	360	365
Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly		
370	375	380
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala		
385	390	395
Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr		
405	410	415
Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu		
420	425	430
Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu		
435	440	445
Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn		
450	455	460
Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg		
465	470	475
Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp		
485	490	495

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
 500 505

<210> 18
 <211> 509
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Lck-TQ

<400> 18

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
 145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
 165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
 180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
260 265 270

Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
275 280 285

Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
290 295 300

Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Gln Glu Tyr Met Glu
305 310 315 320

Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
 450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
 465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
 485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
 500 505

<210> 19

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lck-YF

<400> 19

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro

130

135

140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
 145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
 165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
 180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
 195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
 210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
 225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
 245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
 260 265 270

Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
 275 280 285

Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
 290 295 300

Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu
 305 310 315 320

Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
 325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
 340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
 370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro
500 505

<210> 20
<211> 509
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: Lck-TQ/YF

<400> 20

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
260 265 270

Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
275 280 285

Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
290 295 300

Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Gln Glu Tyr Met Glu
305 310 315 320

Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
 340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
 370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
 405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
 420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
 435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
 450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
 465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
 485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro
 500 505

<210> 21

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Hck-KA

<400> 21

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu
 1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly

20	25	30
Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro		
35	40	45
Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser		
50	55	60
His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile		
65	70	75
Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu		
85	90	95
Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu		
100	105	110
Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro		
115	120	125
Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe		
130	135	140
Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro		
145	150	155
Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys		
165	170	175
Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp		
180	185	190
Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr		
195	200	205
Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His		
210	215	220
Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys		
225	230	235
Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile		
245	250	255
Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe		
260	265	270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val
 275 280 285

Ala Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu
 290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His
 305 310 315 320

Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala
 325 330 335

Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln
 340 345 350

Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met
 355 360 365

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 370 375 380

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly
 385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser
 420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
 435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu
 450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn
 465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg
 485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 515 520 525

<210> 22
<211> 525
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: Hck-TQ

<400> 22

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu
1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly
20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro
35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser
50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile
65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu
85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu
100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro
115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe
130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys
165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp
180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr
195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His
 210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys
 225 230 235 240

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile
 245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe
 260 265 270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val
 275 280 285

Ala Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu
 290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His
 305 310 315 320

Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Gln Glu Phe Met Ala
 325 330 335

Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln
 340 345 350

Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met
 355 360 365

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 370 375 380

Asn Ile Leu Val Ser Ala Ser Leu Val ~~Asp Lys Thr Thr Thr~~ Phe Gly
 385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser
 420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
 435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu

450

455

460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn
 465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg
 485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 515 520 525

<210> 23
 <211> 525
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Hck-YF

<400> 23

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu
 1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly
 20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro
 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser
 50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile
 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu
 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu
 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro
 115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe
 130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys
 165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp
 180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr
 195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His
 210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys
 225 230 235 240

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile
 245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe
 260 265 270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val
 275 280 285

Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu
 290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His
 305 310 315 320

Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala
 325 330 335

Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln
 340 345 350

Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met
 355 360 365

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 370 375 380

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly
385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser
420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu
450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn
465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg
485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Gln Pro
515 520 525

<210> 24

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Hck-TQ/YF

<400> 24

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu
1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly
20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro
35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser
50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile
65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu
85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu
100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro
115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe
130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys
165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp
180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr
195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His
210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys
225 230 235 240

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile
245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe
260 265 270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val
275 280 285

Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu
290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His

305 310 315 320
 Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Gln Glu Phe Met Ala
 325 330 335
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln
 340 345 350
 Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met
 355 360 365
 Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 370 375 380
 Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly
 385 390 395 400
 Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 405 410 415
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser
 420 425 430
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
 435 440 445
 Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu
 450 455 460
 Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn
 465 470 475 480
 Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg
 485 490 495
 Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
 500 505 510
 Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Gln Pro
 515 520 525

<210> 25

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lyn-KA

<400> 25

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
180 185 190

Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
210 215 220

Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
225 230 235 240

Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
245 250 255

Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
260 265 270

Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
275 280 285

Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
290 295 300

Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
305 310 315 320

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly
325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu
340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg
355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp
370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe
405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn
435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val
450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys
465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu
485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
 500 505 510

<210> 26

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lyn-TQ

<400> 26

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr ~~Leu~~ ~~Gln~~ ~~Thr~~ Glu Glu
 115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
 165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly

180	185	190
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile 195 200 205		
Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys 210 215 220		
Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 225 230 235 240		
Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly 245 250 255		
Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val 260 265 270		
Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu 275 280 285		
Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg 290 295 300		
Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu 305 310 315 320		
Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly 325 330 335		
Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu 340 345 350		
Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 355 360 365		
Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp 370 375 380		
Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 385 390 395 400		
Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe 405 410 415		
Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425 430		

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn
 435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val
 450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys
 465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu
 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
 500 505 510

<210> 27
 <211> 511
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Description of sequence: Lyn-YF

<400> 27

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
 115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
 165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
 180 185 190

Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
 195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
 210 215 220

Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
 225 230 235 240

Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
 245 250 255

Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
 260 265 270

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
 275 280 285

Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
 290 295 300

Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
~~305~~ 310 315 320

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly
 325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu
 340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg
 355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp
 370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe
405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn
435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val
450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys
465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu
485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Gln Pro
500 505 510

<210> 28
<211> 511
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: Lyn-TQ/YF

<400> 28

Met Gly Cys Ile Lys Ser Lys Gly Lys ~~Asp Ser~~ ~~Thr Thr~~ Asp Gly
1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp

65	70	75	80
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His	85	90	95
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe	100	105	110
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu	115	120	125
Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu	130	135	140
Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr	145	150	155
Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His	165	170	175
Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly	180	185	190
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile	195	200	205
Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys	210	215	220
Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp	225	230	235
Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly	245	250	255
Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val	260	265	270
Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu	275	280	285
Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg	290	295	300
Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu	305	310	315
			320

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly
 325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu
 340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg
 355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp
 370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
 385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe
 405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn
 435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val
 450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys
 465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu
 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Gln Pro
 500 505 510

<210> 29

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: BLK-KA

<400> 29

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys
 1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
 20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
 35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
 50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
 65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
 85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
 100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
 115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
 130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
 145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
 165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
 180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
 195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
 210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser
 225 230 235 240

Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp
 245 250 255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Ala Thr Leu Lys
 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met
 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr
 290 295 300

Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu
 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg
 325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile
 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys
 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala
 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu
 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg
 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala
 485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro
 500 505

<211> 505
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: BLK-TQ

<400> 30

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys
1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
 210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser
 225 230 235 240

Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp
 245 250 255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys
 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met
 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr
 290 295 300

Lys Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ala Arg Gly Cys Leu
 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg
 325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile
 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys
 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala
 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu
 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg
465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala
485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro
500 505

<210> 31

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: BLK-YF

<400> 31

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys
1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
 165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
 180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
 195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
 210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser
 225 230 235 240

Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp
 245 250 255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys
 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met
 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr
 290 295 300

Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu
 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg
 325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile
 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys
 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala

405

410

415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu
 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg
 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala
 485 490 495

Thr Glu Arg Gln Phe Glu Leu Gln Pro
 500 505

<210> 32

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Blk-TQ/YF

<400> 32

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys
 1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
 20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
 35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
 50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
 65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
 85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
 100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
 115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
 130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
 145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
 165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
 180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
 195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
 210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser
 225 230 235 240

Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp
 245 250 255

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys
 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met
 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr
 290 295 300

Lys Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ala Arg Gly Cys Leu
 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg
 325 330 335

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile
 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys
 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala
 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu
 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg
 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala
 485 490 495

Thr Glu Arg Gln Phe Glu Leu Gln Pro
 500 505

<210> 33
 <211> 536
 <212> PRT
 <213> Chicken

<221> misc_feature
 <223> Description of sequence: Yrk-KA

<400> 33

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
210 215 220

Gln Leu Val Gln His Tyr Ile Glu ~~Arg Ala Ala Gly Thr~~ Cys Cys Arg
225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Ala Thr Leu Lys Pro Gly Thr

290

295

300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
 370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
 385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
 450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln
 530 535

<210> 34
 <211> 536
 <212> PRT
 <213> Chicken

<220>
 <221> misc_feature
 <223> Description of sequence: Yrk-TQ

<400> 34

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
 50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
 65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
 85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
 100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
 115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
 130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
 145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
 165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
 180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
 195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335

Ile Tyr Ile Val Gln Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln
530 535

<210> 35

<211> 536

<212> PRT

<213> Chicken

<220>

<221> misc_feature

<223> Description of sequence: Yrk-YF

<400> 35

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala

115

120

125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
 130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
 145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
 165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
 180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
 195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
 210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
 225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
 245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
 260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
 275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
 290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln
530 535

<210> 36

<211> 536

<212> PRT

<213> Chicken

<220>

<221> misc_feature

<223> Description of sequence: Yrk-TQ/YF

<400> 36

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
 290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

Ile Tyr Ile Val Gln Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
 370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
 385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
 450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln

530

535

<210> 37
 <211> 536
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Src kinase (Fig. 18)

<220>
 <221> SITE
 <222> (298)
 <223> Constant amino acid K in domain SH2

<220>
 <221> SITE
 <222> (341)
 <223> Constant amino acid T in domain SH2

<220>
 <221> SITE
 <222> (530)
 <223> Constant amino acid Y in domain SH1

<400> 37
 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 38
<211> 543
<212> PRT
<213> Homo sapiens

<220>
<223> Yes kinase (Fig. 18)

<220>
<221> SITE
<222> (305)
<223> Constant amino acid K in domain SH2

<220>
<221> SITE
<222> (348)
<223> Constant amino acid T in domain SH2

<220>
<221> SITE
<222> (537)
<223> Constant amino acid Y in domain SH1

<400> 38
Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly

				180				185				190			
Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Glu	Ile	Arg	Gly	Asp	Asn
		195					200					205			
Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Asn	Gly	Gly	Tyr	Tyr	Ile
		210				215						220			
Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Leu	Gln	Lys	Leu	Val	Lys	His	Tyr
225				230						235					
Thr	Glu	His	Ala	Asp	Gly	Leu	Cys	His	Lys	Leu	Thr	Thr	Val	Cys	Pro
				245				250						255	
Thr	Val	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile
			260					265					270		
Pro	Arg	Glu	Ser	Leu	Arg	Leu	Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe
		275					280					285			
Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Ile
		290				295				300					
Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Met	Pro	Glu	Ala	Phe	Leu	Gln	Glu
305				310						315					
Ala	Gln	Ile	Met	Lys	Lys	Leu	Arg	His	Asp	Lys	Leu	Val	Pro	Leu	Tyr
				325				330						335	
Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser
			340					345				350			
Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Glu	Gly	Asp	Gly	Lys	Tyr	Leu
		355					360					365			
Lys	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Ile	Ala	Asp	Gly	Met
		370				375				380					
Ala	Tyr	Ile	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala
385				390						395					
Asn	Ile	Leu	Val	Gly	Glu	Asn	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly
				405				410						415	
Leu	Ala	Arg	Leu	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala
			420					425					430		
Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg
		435					440					445			
Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Gln	Thr	Glu
		450				455				460					
Leu	Val	Thr	Lys	Gly	Arg	Val	Pro	Tyr	Pro	Gly	Met	Val	Asn	Arg	Glu
465				470						475					
Val	Leu	Glu	Gln	Val	Glu	Arg	Gly	Tyr	Arg	Met	Pro	Cys	Pro	Gln	Gly
			485					490						495	
Cys	Pro	Glu	Ser	Leu	His	Glu	Leu	Met	Asn	Leu	Cys	Trp	Lys	Lys	Asp
			500					505					510		
Pro	Asp	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Phe	Leu	Glu	Asp

515

520

525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 39

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> Fyn kinase (Fig. 18)

<220>

<221> SITE

<222> (299)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (342)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (531)

<223> Constant amino acid Y in domain SH1

<400> 39

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
 85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
 115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
 130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
 145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
 165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
 180 185 190
 Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
 195 200 205
 Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
 210 215 220
 Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
 225 230 235 240
 Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
 245 250 255
 Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
 260 265 270
 Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285
 Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300
 Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320
 Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335
 Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350
 Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365
 Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380
 Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400
 Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415
 Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445
 Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460
 Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480
 Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495
 Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 40

<211> 536

<212> PRT

<213> Chicken

<220>

<223> Yrk kinase (Fig. 18)

<220>

<221> SITE

<222> (298)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (341)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (530)

<223> Constant amino acid Y in domain SH1

<400> 40

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335

Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln
 530 535

<210> 41
 <211> 529
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Fgr kinase (Fig. 18)

<220>
 <221> SITE
 <222> (291)
 <223> Constant amino acid K in domain SH2

<220>
 <221> SITE
 <222> (334)
 <223> Constant amino acid T in domain SH2

<220>
 <221> SITE
 <222> (523)
 <223> Constant amino acid Y in domain SH1

<400> 41
 Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45
 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60
 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80
 Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95
 Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
 100 105 110
 Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
 115 120 125
 Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
 130 135 140
 Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
 145 150 155 160
 Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr

165										170					175				
Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Gln	Thr	Arg	Gly				
			180					185					190						
Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Met	Gly	Gly	Tyr				
		195					200					205							
Tyr	Ile	Thr	Thr	Arg	Val	Gln	Phe	Asn	Ser	Val	Gln	Glu	Leu	Val	Gln				
	210					215					220								
His	Tyr	Met	Glu	Val	Asn	Asp	Gly	Leu	Cys	Asn	Leu	Leu	Ile	Ala	Pro				
225					230					235					240				
Cys	Thr	Ile	Met	Lys	Pro	Gln	Thr	Leu	Gly	Leu	Ala	Lys	Asp	Ala	Trp				
				245					250						255				
Glu	Ile	Ser	Arg	Ser	Ser	Ile	Thr	Leu	Glu	Arg	Arg	Leu	Gly	Thr	Gly				
			260					265						270					
Cys	Phe	Gly	Asp	Val	Trp	Leu	Gly	Thr	Trp	Asn	Gly	Ser	Thr	Lys	Val				
		275					280					285							
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Lys	Ala	Phe	Leu				
	290					295					300								
Glu	Glu	Ala	Gln	Val	Met	Lys	Leu	Leu	Arg	His	Asp	Lys	Leu	Val	Gln				
305					310					315					320				
Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe				
				325					330						335				
Met	Cys	His	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Asn	Pro	Glu	Gly	Gln				
			340					345						350					
Asp	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Val	Ala	Glu				
		355					360						365						
Gly	Met	Ala	Tyr	Met	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg				
	370					375					380								
Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Arg	Leu	Ala	Cys	Lys	Ile	Ala	Asp				
385					390					395					400				
Phe	Gly	Leu	Ala	Arg	Leu	Ile	Lys	Asp	Asp	Glu	Tyr	Asn	Pro	Cys	Gln				
				405					410						415				
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Phe				
			420					425						430					
Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu				
		435					440					445							
Thr	Glu	Leu	Ile	Thr	Lys	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Asn	Lys				
	450					455					460								
Arg	Glu	Val	Leu	Glu	Gln	Val	Glu	Gln	Gly	Tyr	His	Met	Pro	Cys	Pro				
465					470					475					480				
Pro	Gly	Cys	Pro	Ala	Ser	Leu	Tyr	Glu	Ala	Met	Glu	Gln	Thr	Trp	Arg				
				485					490						495				
Leu	Asp	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu				

500

505

510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln
 515 520 525

Thr

<210> 42

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<223> Hck kinase (Fig. 18)

<220>

<221> SITE

<222> (289)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (332)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (525)

<223> Constant amino acid Y in domain SH1

<400> 42

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu
 1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly
 20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro
 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser
 50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile
 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu
 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu
 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro
 115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe
 130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys
 165 170 175
 Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp
 180 185 190
 Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr
 195 200 205
 Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His
 210 215 220
 Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys
 225 230 235 240
 Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile
 245 250 255
 Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe
 260 265 270
 Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val
 275 280 285
 Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu
 290 295 300
 Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His
 305 310 315 320
 Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala
 325 330 335
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln
 340 345 350
 Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met
 355 360 365
 Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 370 375 380
 Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly
 385 390 395 400
 Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 405 410 415
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser
 420 425 430
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
 435 440 445
 Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu
 450 455 460
 Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn
 465 470 475 480
 Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg
 485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 515 520 525

<210> 43

<211> 512

<212> PRT

<213> Homo sapiens

<220>

<223> Lyn kinase (Fig. 18)

<220>

<221> SITE

<222> (275)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (319)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (508)

<223> Constant amino acid Y in domain SH1

<400> 43

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
 115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
 165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
 180 185 190
 Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
 195 200 205
 Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
 210 215 220
 Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
 225 230 235 240
 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
 245 250 255
 Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
 260 265 270
 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
 275 280 285
 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
 290 295 300
 Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
 305 310 315 320
 Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly
 325 330 335
 Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala
 340 345 350
 Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu
 355 360 365
 Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala
 370 375 380
 Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg
 385 390 395 400
 Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn
 405 410 415
 Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
 420 425 430
 Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr
 435 440 445
 Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg
 450 455 460
 Val Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp
 465 470 475 480
 Lys Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val
 485 490 495
 Leu Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
 500 505 510

<210> 44
 <211> 509
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Lck kinase (Fig. 18)

<220>
 <221> SITE
 <222> (273)
 <223> Constant amino acid K in domain SH2

<220>
 <221> SITE
 <222> (316)
 <223> Constant amino acid T in domain SH2

<220>
 <221> SITE
 <222> (505)
 <223> Constant amino acid Y in domain SH1

<400> 44
 Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
 1 5 10 15
 Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
 20 25 30
 Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45
 Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
 50 55 60
 Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
 65 70 75 80
 Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
 85 90 95
 Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
 100 105 110
 Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
 115 120 125
 Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 130 135 140
 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
 145 150 155 160
 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
 165 170 175
 Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
 180 185 190
 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His

195	200	205
Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys 210 215 220		
Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val 225 230 235 240		
Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe 245 250 255		
Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val 260 265 270		
Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu 275 280 285		
Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr 290 295 300		
Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu 305 310 315 320		
Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu 325 330 335		
Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 340 345 350		
Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 355 360 365		
Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly 370 375 380		
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 385 390 395 400		
Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 415		
Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 430		
Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 435 440 445		
Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 450 455 460		
Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 465 470 475 480		
Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp 485 490 495		
Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro 500 505		

<210> 45

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<223> Blk kinase (Fig. 18)

<220>

<221> SITE

<222> (269)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (312)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (501)

<223> Constant amino acid Y in domain SH1

<400> 45

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys
1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
195 200 205

Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
210 215 220

Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser
 225 230 235 240
 Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp
 245 250 255
 Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys
 260 265 270
 Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met
 275 280 285
 Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr
 290 295 300
 Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu
 305 310 315 320
 Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg
 325 330 335
 Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
 340 345 350
 Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365
 Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile
 370 375 380
 Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys
 385 390 395 400
 Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala
 405 410 415
 Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
 420 425 430
 Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
 435 440 445
 Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu
 450 455 460
 Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg
 465 470 475 480
 Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala
 485 490 495
 Thr Glu Arg Gln Tyr Glu Leu Gln Pro
 500 505

<210> 46

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide (sense) used for the generation of

Src-K298A (page 35 of description)

<400> 46

ccagggtggc catgccacc ctgaagcctg gcac

34

<210> 47

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide (antisense) used for the
generation of Src-K298A (page 35 of description)

<400> 47

gtgccaggct tcagggtggc gatggccacc ctgg

34

<210> 48

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide (sense) used for the generation of
Src-T341Q (page 35 of description)

<400> 48

ccatttacat cgtccaggag tacatgagca ag

32

<210> 49

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide (antisense) used for the
generation of Src-T341Q (page 35 of description)

<400> 49

cttgctcatg tactcctgga cgatgtaaat gg

32

<210> 50

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide (sense) used for the generation of
Src-Y530F (page 35 of description)

<400> 50

ccaccgagcc ccagttccag cccggggag

29

<210> 51

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide (antisense) used for the
generation of Src-Y530F (page 35 of description)

<400> 51

ctccccgggc tggaactggg gctcggtgg

29